

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/500,671A
Source: PGT/10
Date Processed by STIC: 3/22/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/22/2005

PATENT APPLICATION: US/10/500,671A

TIME: 10:15:49

Input Set : E:\1392-10-18-2 revised sequence.ST25.txt

Output Set: N:\CRF4\03222005\J500671A.raw

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3 <110> APPLICANT: Sera, Takashi
5 <120> TITLE OF INVENTION: Nuclear-Envelope and Nuclear-Lamina Binding Chimeras for
6   Modulating Gene Expression
8 <130> FILE REFERENCE: 109845-163
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/500,671A
C--> 10 <141> CURRENT FILING DATE: 2004-07-02
10 <160> NUMBER OF SEQ ID NOS: 21
12 <170> SOFTWARE: PatentIn version 3.3
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 25
16 <212> TYPE: PRT
17 <213> ORGANISM: Artificial
19 <220> FEATURE:
20 <223> OTHER INFORMATION: Zinc finger domain
23 <220> FEATURE:
24 <221> NAME/KEY: MISC_FEATURE
25 <222> LOCATION: (2)..(5)
26 <223> OTHER INFORMATION: Amino acids 2-5 are Xaa wherein Xaa = any amino acid, and up
to
27   two amino acids can be missing.
29 <220> FEATURE:
30 <221> NAME/KEY: MISC_FEATURE
31 <222> LOCATION: (7)..(18)
32 <223> OTHER INFORMATION: Xaa can be any amino acid
34 <220> FEATURE:
35 <221> NAME/KEY: MISC_FEATURE
36 <222> LOCATION: (20)..(24)
37 <223> OTHER INFORMATION: Amino acids 20-24 are Xaa wherein Xaa = any amino acid, and
up to
38   two amino acids can be missing.
40 <400> SEQUENCE: 1
W--> 42 Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
43 1           5           10           15
46 Xaa Xaa His Xaa Xaa Xaa Xaa His
47           20           25
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 32
52 <212> TYPE: PRT
53 <213> ORGANISM: Artificial
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Second zinc finger domain
59 <220> FEATURE:
60 <221> NAME/KEY: MISC_FEATURE
61 <222> LOCATION: (1)..(3)

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62 <223> OTHER INFORMATION: Xaa can be any amino acid

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64 <220> FEATURE:
 65 <221> NAME/KEY: MISC_FEATURE
 66 <222> LOCATION: (5)..(8)
 67 <223> OTHER INFORMATION: Amino acids 5-8 are Xaa wherein Xaa = any amino acid, and up
 to
 68 two amino acids can be missing
 70 <220> FEATURE:
 71 <221> NAME/KEY: MISC_FEATURE
 72 <222> LOCATION: (10)..(14)
 73 <223> OTHER INFORMATION: Xaa can be any amino acid
 75 <220> FEATURE:
 76 <221> NAME/KEY: MISC_FEATURE
 77 <222> LOCATION: (15)..(15)
 78 <223> OTHER INFORMATION: Amino acid 15 is Z(-1) wherein Z(-1) = Arg, Lys, Gln, Asn,
 Thr,
 79 Met, Leu, Ile, Glu or Asp.
 81 <220> FEATURE:
 82 <221> NAME/KEY: MISC_FEATURE
 83 <222> LOCATION: (16)..(16)
 84 <223> OTHER INFORMATION: Xaa can be any amino acid
 86 <220> FEATURE:
 87 <221> NAME/KEY: MISC_FEATURE
 88 <222> LOCATION: (17)..(17)
 89 <223> OTHER INFORMATION: Amino acid 17 is Z2 wherein Z2 = Ser, Arg, Asn, Gln, Thr,
 Val,
 90 Ala, Asp or Glu.
 92 <220> FEATURE:
 93 <221> NAME/KEY: MISC_FEATURE
 94 <222> LOCATION: (18)..(18)
 95 <223> OTHER INFORMATION: Amino acid 18 is Z3 wherein Z3 = His, Lys, Asn, Gln, Ser,
 Ala,
 96 Val, Thr, Asp, or Glu
 98 <220> FEATURE:
 99 <221> NAME/KEY: MISC_FEATURE
 100 <222> LOCATION: (19)..(20)
 101 <223> OTHER INFORMATION: Xaa can be any amino acid
 103 <220> FEATURE:
 104 <221> NAME/KEY: MISC_FEATURE
 105 <222> LOCATION: (21)..(21)
 106 <223> OTHER INFORMATION: Amino acid 21 is Z6 wherein Z6 = Arg, Lys, Gln, Asn, Thr,
 Tyr,
 107 Leu, Ile, Met, Glu or Asp.
 109 <220> FEATURE:
 110 <221> NAME/KEY: MISC_FEATURE
 111 <222> LOCATION: (23)..(27)
 112 <223> OTHER INFORMATION: Amino acids 23-27 are Xaa wherein Xaa = any amino acid, and
 up to
 113 two amino acids can be missing.
 115 <220> FEATURE:
 116 <221> NAME/KEY: MISC_FEATURE
 117 <222> LOCATION: (29)..(32)
 118 <223> OTHER INFORMATION: Xaa can be any amino acid
 120 <400> SEQUENCE: 2

W--> 122 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 123 1 5 10 15

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126 Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa
127          20          25          30
130 <210> SEQ ID NO: 3
131 <211> LENGTH: 28
132 <212> TYPE: PRT
133 <213> ORGANISM: Artificial
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Zinc finger domain
139 <220> FEATURE:
140 <221> NAME/KEY: MISC_FEATURE
141 <222> LOCATION: (13)..(13)
142 <223> OTHER INFORMATION: Amino acid 13 is Z(-1) wherein Z(-1) = Arg, Lys, Gln, Asn,
Thr,
143      Met, Leu, Ile, Glu or Asp.
145 <220> FEATURE:
146 <221> NAME/KEY: MISC_FEATURE
147 <222> LOCATION: (15)..(15)
148 <223> OTHER INFORMATION: Amino acid 15 is Z2 wherein Z2 = Ser, Arg, Asn, Gln, Thr,
Val,
149      Ala, Asp or Glu.
151 <220> FEATURE:
152 <221> NAME/KEY: MISC_FEATURE
153 <222> LOCATION: (16)..(16)
154 <223> OTHER INFORMATION: Amino acid 16 is Z3 wherein Z3 = His, Lys, Asn, Gln, Ser,
Ala,
155      Val, Thr, Asp or Glu.
157 <220> FEATURE:
158 <221> NAME/KEY: MISC_FEATURE
159 <222> LOCATION: (19)..(19)
160 <223> OTHER INFORMATION: Amino acid 19 is Z6 wherein Z6 = Arg, Lys, Gln, Asn, Thr,
Tyr,
161      Leu, Ile, Met, Glu or Asp.
163 <400> SEQUENCE: 3
W--> 165 Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Xaa Ser Xaa Xaa
166 1          5          10          15
169 Leu Gln Xaa His Gln Arg Thr His Thr Gly Glu Lys
170          20          25
173 <210> SEQ ID NO: 4
174 <211> LENGTH: 5
175 <212> TYPE: PRT
176 <213> ORGANISM: Artificial
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Synthetic flexible linker peptide for linking together
180      multi-finger zinc finger domains
182 <400> SEQUENCE: 4
184 Gly Gly Gly Gly Ser
185 1          5
188 <210> SEQ ID NO: 5
189 <211> LENGTH: 11
190 <212> TYPE: PRT
191 <213> ORGANISM: Human immunodeficiency virus
194 <220> FEATURE:
195 <221> NAME/KEY: MISC_FEATURE

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196 <222> LOCATION: (1)..(11)
197 <223> OTHER INFORMATION: HIV Tat protein domain
199 <400> SEQUENCE: 5
201 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
202 1          5          10
205 <210> SEQ ID NO: 6
206 <211> LENGTH: 9
207 <212> TYPE: DNA
208 <213> ORGANISM: Human immunodeficiency virus
211 <220> FEATURE:
212 <221> NAME/KEY: misc_feature
213 <222> LOCATION: (1)..(9)
214 <223> OTHER INFORMATION: HIV DNA Binding Domain
216 <400> SEQUENCE: 6
217 gcagaagcc
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 19
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial
225 <220> FEATURE:
226 <223> OTHER INFORMATION: DNA target sequence
228 <400> SEQUENCE: 7
229 gtgtgggtga gtgagtgtg
232 <210> SEQ ID NO: 8
233 <211> LENGTH: 19
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial
237 <220> FEATURE:
238 <223> OTHER INFORMATION: DNA target sequence
240 <400> SEQUENCE: 8
241 ggggctgggg gcggtgtct
244 <210> SEQ ID NO: 9
245 <211> LENGTH: 7
246 <212> TYPE: PRT
247 <213> ORGANISM: Simian virus 40
250 <220> FEATURE:
251 <221> NAME/KEY: MISC_FEATURE
252 <222> LOCATION: (1)..(7)
253 <223> OTHER INFORMATION: Peptide from SV40 large T antigen
255 <400> SEQUENCE: 9
257 Pro Lys Lys Lys Arg Lys Val
258 1          5
261 <210> SEQ ID NO: 10
262 <211> LENGTH: 16
263 <212> TYPE: PRT
264 <213> ORGANISM: Artificial
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Peptide, residues 43-58 of the Antennapeida homeodomain
protein
270 <220> FEATURE:

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271 <221> NAME/KEY: MISC_FEATURE
272 <222> LOCATION: (1)..(16)
273 <223> OTHER INFORMATION: Peptide, residues 43-58 of the Antennapeida homeodomain
protein
275 <400> SEQUENCE: 10
277 Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
278 1          5          10          15
281 <210> SEQ ID NO: 11
282 <211> LENGTH: 34
283 <212> TYPE: PRT
284 <213> ORGANISM: Herpes Simplex Virus
287 <220> FEATURE:
288 <221> NAME/KEY: MISC_FEATURE
289 <222> LOCATION: (1)..(34)
290 <223> OTHER INFORMATION: Residues 267-300 of the HSV VP22 protein
292 <400> SEQUENCE: 11
294 Asp Ala Ala Thr Ala Thr Arg Gly Arg Ser Ala Ala Ser Arg Pro Thr
295 1          5          10          15
298 Glu Arg Pro Arg Ala Pro Ala Arg Ser Ala Ser Arg Pro Arg Arg Pro
299          20          25          30
302 Val Glu
306 <210> SEQ ID NO: 12
307 <211> LENGTH: 11
308 <212> TYPE: PRT
309 <213> ORGANISM: Artificial
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Synthetic peptide modeled after the protein transduction
domain
313 of the human immunodeficiency virus TAT protein having cellular
314 uptake activity
316 <400> SEQUENCE: 12
318 Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
319 1          5          10
322 <210> SEQ ID NO: 13
323 <211> LENGTH: 9
324 <212> TYPE: PRT
325 <213> ORGANISM: Artificial
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Synthetic peptide modeled after the protein transduction
domain
329 of the human immunodeficiency virus TAT protein having cellular
330 uptake activity, referred to as "R9"
332 <400> SEQUENCE: 13
334 Arg Arg Arg Arg Arg Arg Arg Arg
335 1          5
338 <210> SEQ ID NO: 14
339 <211> LENGTH: 16
340 <212> TYPE: PRT
341 <213> ORGANISM: Artificial
343 <220> FEATURE:
344 <223> OTHER INFORMATION: D-penetratin peptide
347 <220> FEATURE:

```


RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/22/2005
PATENT APPLICATION: US/10/500,671A TIME: 10:15:50

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. ~~2,3,4,5,7,8,9,10,11,12,13,14,15,16,17,18,20,21,22,23,24~~
Seq#:2; Xaa Pos. ~~1,2,3,5,6,7,8,10,11,12,13,14,15,16,17,18,19,20,21,23,24,25~~
Seq#:2; Xaa Pos. ~~26,27,29,30,31,32~~
Seq#:3; Xaa Pos. ~~1,3,15,16,19~~

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,7,8,10,12,13,14,15,16,17,18,19,20,21

VERIFICATION SUMMARY

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Input Set : E:\1392-10-18-2 revised sequence.ST25.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
M:341 Repeated in SeqNo=1
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:341 Repeated in SeqNo=2
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:341 Repeated in SeqNo=3